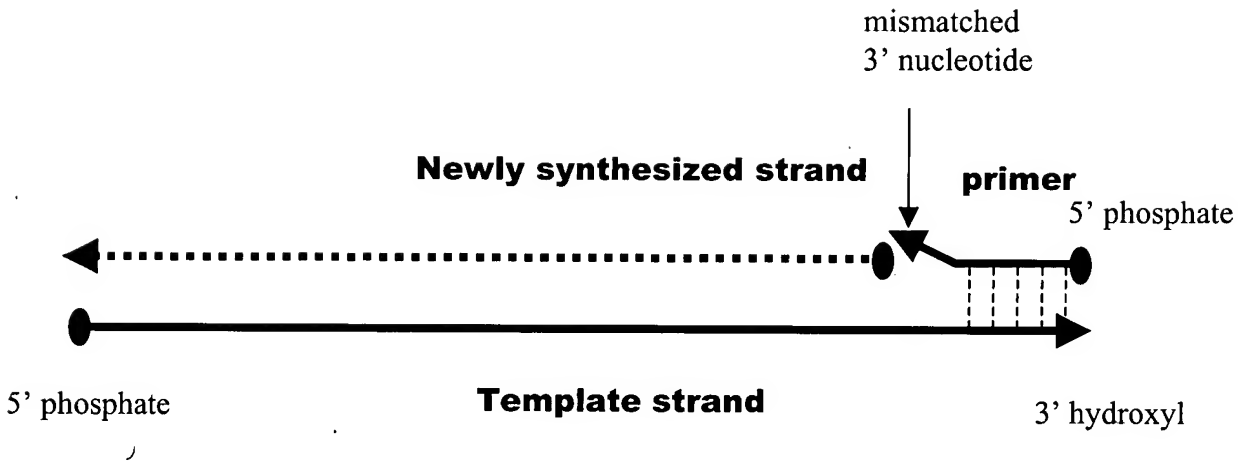
mismatched
3' nucleotide
Newly synthesized strand
primer
5' phosphate
5' phosphate
Template strand
3' hydroxyl

Figure 1

CLUSTAL W(1.4) multiple sequence alignment of
FOX C2 RT (SEQ ID NO:1) and FOX C3 RT (SEQ ID NO:2)

```
FOX C2 RT   MNQISKNDSLDVLQDEMGQKKTFESERKSLSGWDYFKSLGSIGRLPHFSRGIELREVKKA 60
            ****************.************ ****************** **.**.***.*
FOX C3 RT   MNQISKNDSLDVLQDEIGQKKTFESERKSSSGWDYFKSLGSIGRLPHFNRGMELKEVKRA 60

FOX C2 RT   NRYLAFQEQRIVSAIEAGEIRKAVLVWLCLMKVSRSYQILLFNRVCKGWYWRWSTARVEE 120
            ********.***.*.* ***************.**********************.*****
FOX C3 RT   NRYLAFQEKRIVTAVEQGEIRKAVLVWLCLMKISRSYQILLFNRVCKGWYWRWSSARVEE 120

FOX C2 RT   IIFGAMNKMRSWDMKLLIHRFYILKKNGKMRPIGAPNYESRMISKALTDMLYSITEKSRS 180
            .*********.*************************************.**..******
FOX C3 RT   VIFGAMNKMRAWDMKLLIHRFYILKKNGKMRPIGAPNYESRMISKALTDLLYTVTEKSRS 180

FOX C2 RT   AEQHGYMKKRGAWSAILECLSKLKEGYAGYEFDLKSFFNTVEPFIYFRKLEEVDKKLTKL 240
            ************************************************************.
FOX C3 RT   AEQHGYMKKRGAWSAILECLSKLKEGYAGYEFDLKSFFNTVEPFIYFRKLEEVDKKLTKV 240

FOX C2 RT   ISNVIKGIEYRFSELLPESELNPKANRKNTLERTGVPQGLSLSPLLSTWALEYYGRPENL 300
            ************.***********  ***** ****************************
FOX C3 RT   ISNVIKGIEYRFTELLPESELNPKGKRKNTLVRTGVPQGLSLSPLLSTWALEYYGRPENL 300

FOX C2 RT   IMYADDGIYFFKHNISKFTRWIERMGRAGIEISPEKSGSLTPVFKFCGVTIDQPKRLVTY 360
            ***********.*********.*** ******.******* ******** *** ******
FOX C3 RT   IMYADDGIYFFRHNISKFTRWLERMSRAGIEIAPEKSGSLKPVFKFCGVEIDQVKRLVTY 360

FOX C2 RT   EGQSVSWDNPELEKWLKSINNLGYTKKEPEWSWTVNGESFITKRKLNLTWMEIVKVYWFR 420
            . ********.** *****.***************   .***** **.****  .******
FOX C3 RT   DKQSVSWDNPDLEPWLKSIHNLGYTKKEPEWSWTVDQNAFITKRNLNITWMETLKVYWFR 420

FOX C2 RT   IIHGKMWNGYTVFLASGWRILDIFGSSSWACNELLMEVKRRREELESIKTFGLEKAEYEA 480
            *. ***********.****.*********.*****  .* *. ******.**********
FOX C3 RT   IVEGKMWNGYTVFLTSGWRVLDIFGSSSWSCNELLKIIKERKNELESIKAFGLEKAEYEA 480

FOX C2 RT   FSYAPVRKGSYRRHYNNGAQETANKQEYWEIMQFHNLKRQQLRAIIE              527
            ******************  * *********.****.*********
FOX C3 RT   FSYAPVRKGSYRRHYNNGAPKTVNKQEYWEIMEFHNLRRQQLRAIIE              527
```

Figure 2

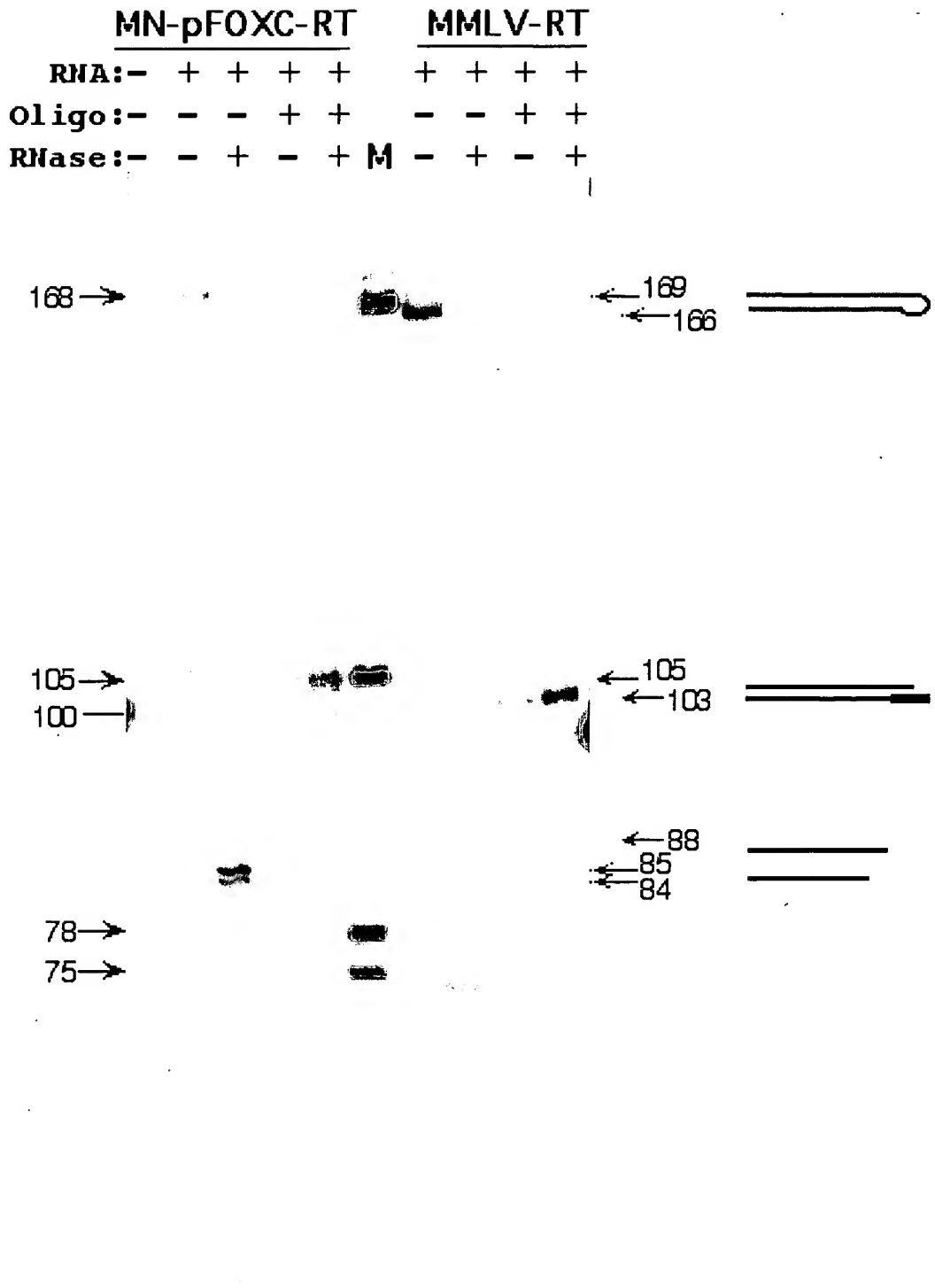

Figure 3

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A

dA*
3R*
+ dCGT dCT
+ ddT ddG

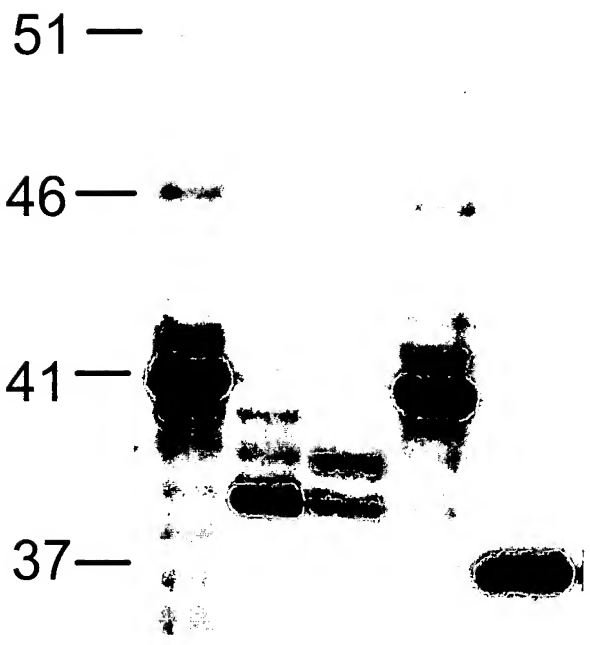

Figure 4

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B

3R oligo (37 nt)

```
3'  GGTTAATCAGATCTAGATTAGATTAGATGTACCTAGG 5'
5'  |||  ||| :|||||: :|||||: |||  |||
```

	Nts in Rx	(Size)
GGATCCATGTAGATTAGATTAGATCTAGACTAATTGGatcc	dA* + dCGT	(41)
GGATCCATGTAGATTAGATTAGATCTAGACTAATTGGa	dA*	(38)
GGATCCATGTAGATTAGATTAGATCTAGACTAATTGGat	dA* + ddT	(39)
GGATCCATGTAGATTAGATTAGATCTAGACTAATTGGatcc	dA*+ dCT + ddG	(41)

```
3'       GGTTAATCAGATCTAGATTAGATTAGATGTACCTAGG 5'
5'       : :|||||  :|||||||||: |||||: :
```

GGATCCATGTAGATTAGATTAGATCTAGACTAATTGGcatggatcc	dA*+ dCGT	(46)
GGATCCATGTAGATTAGATTAGATCTAGACTAATTGG	dA*	(-)
GGATCCATGTAGATTAGATTAGATCTAGACTAATTGG	dA*+ ddT	(-)
GGATCCATGTAGATTAGATTAGATCTAGACTAATTGGcatg	dA*+ dCT + ddG	(41)

```
              GGTTAATC-AGATCTAGATTAGATTAGATGTACCTAGG 5'
              : :|||||  ||||||  |||||: :
```

GGATCCATGTAGATTAGATTAGATCTAGA-CTAATTGGatctacatggatcc	dA* + dCGT	(51)
GGATCCATGTAGATTAGATTAGATCTAGA-CTAATTGGa	dA*	(38)
GGATCCATGTAGATTAGATTAGATCTAGA-CTAATTGGat	dA* + ddT	(39)
GGATCCATGTAGATTAGATTAGATCTAGA-CTAATTGGatcatcatg	dA* + dCT + ddG	(46)

Figure 4

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Figure 5

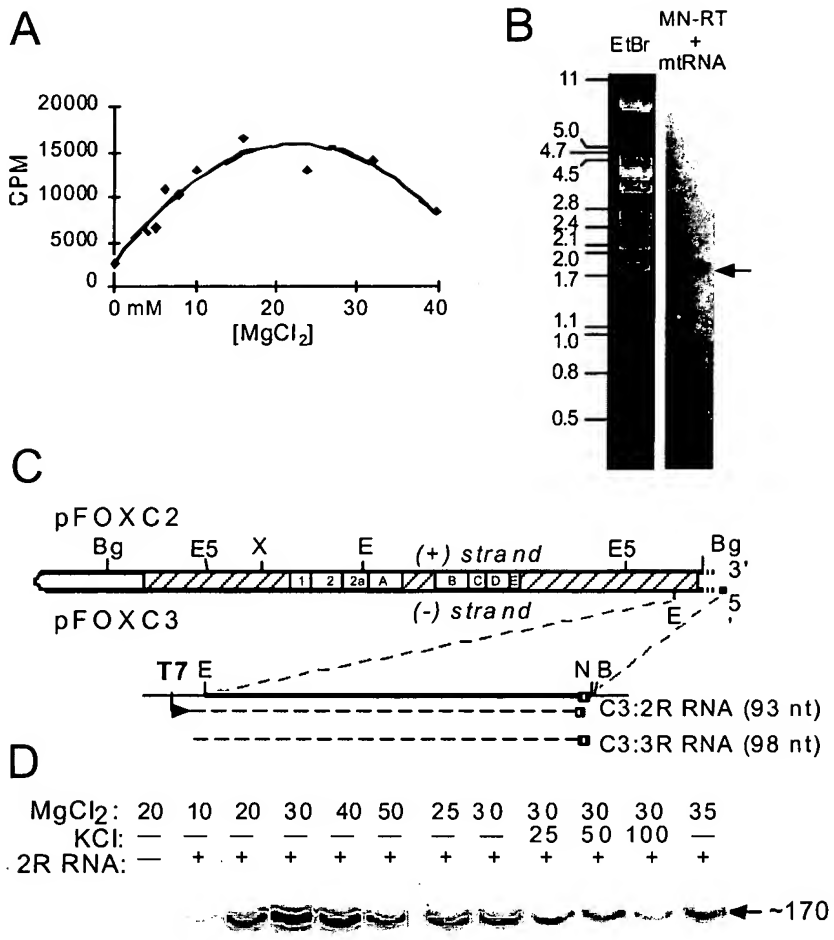

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Figure 6

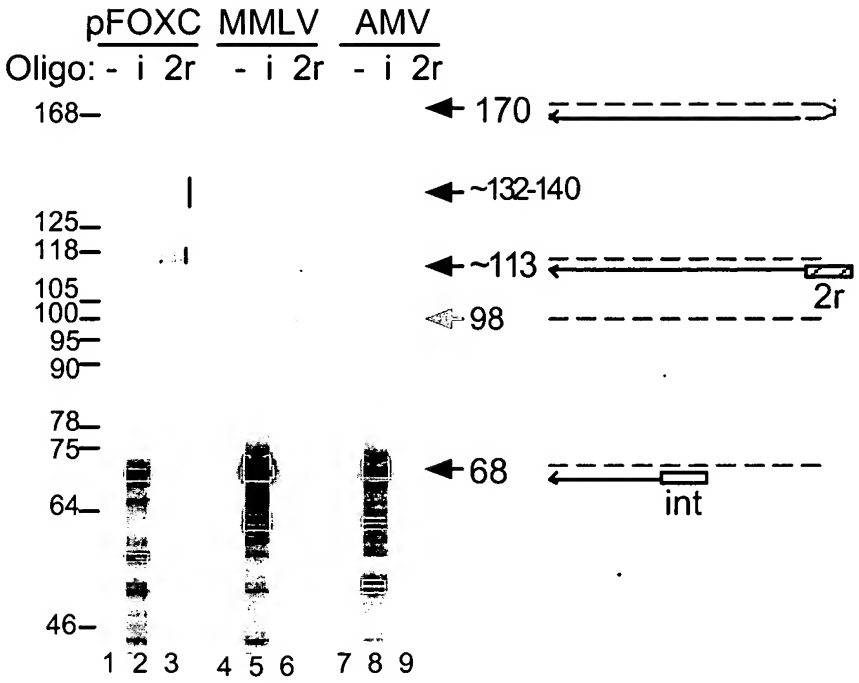

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Figure 7

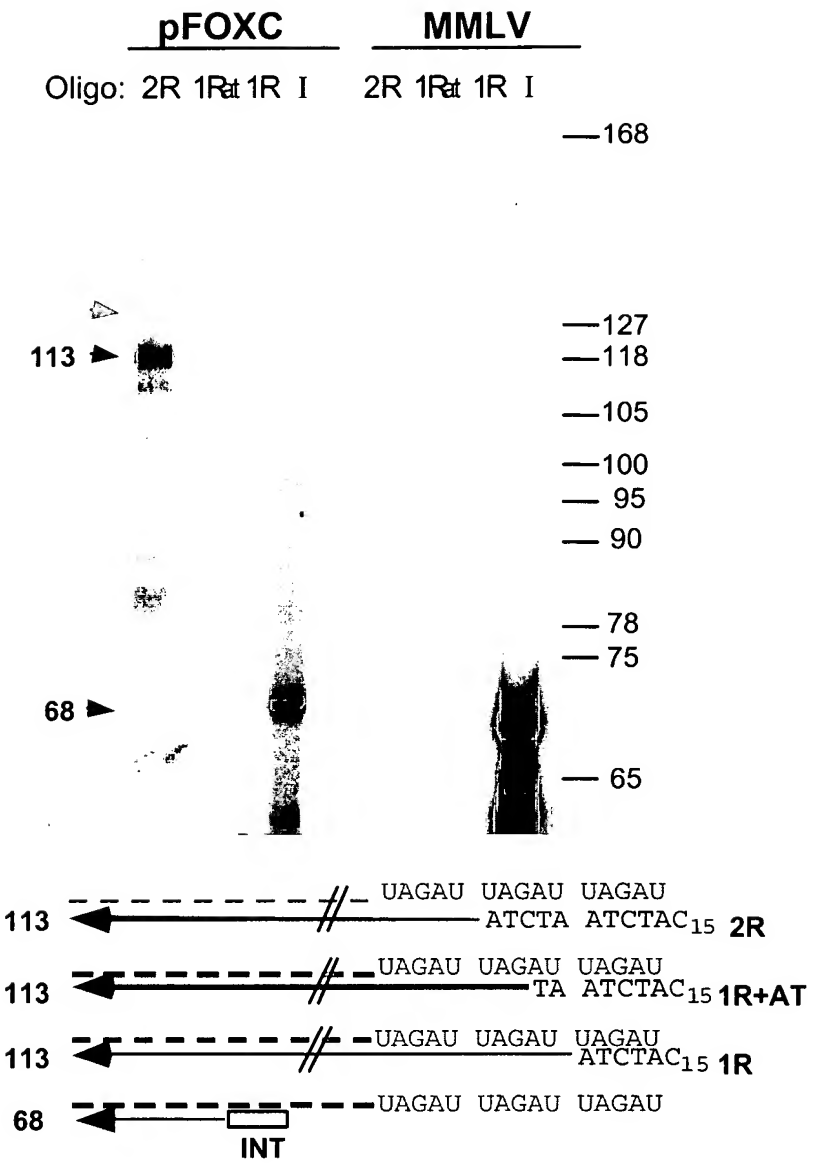

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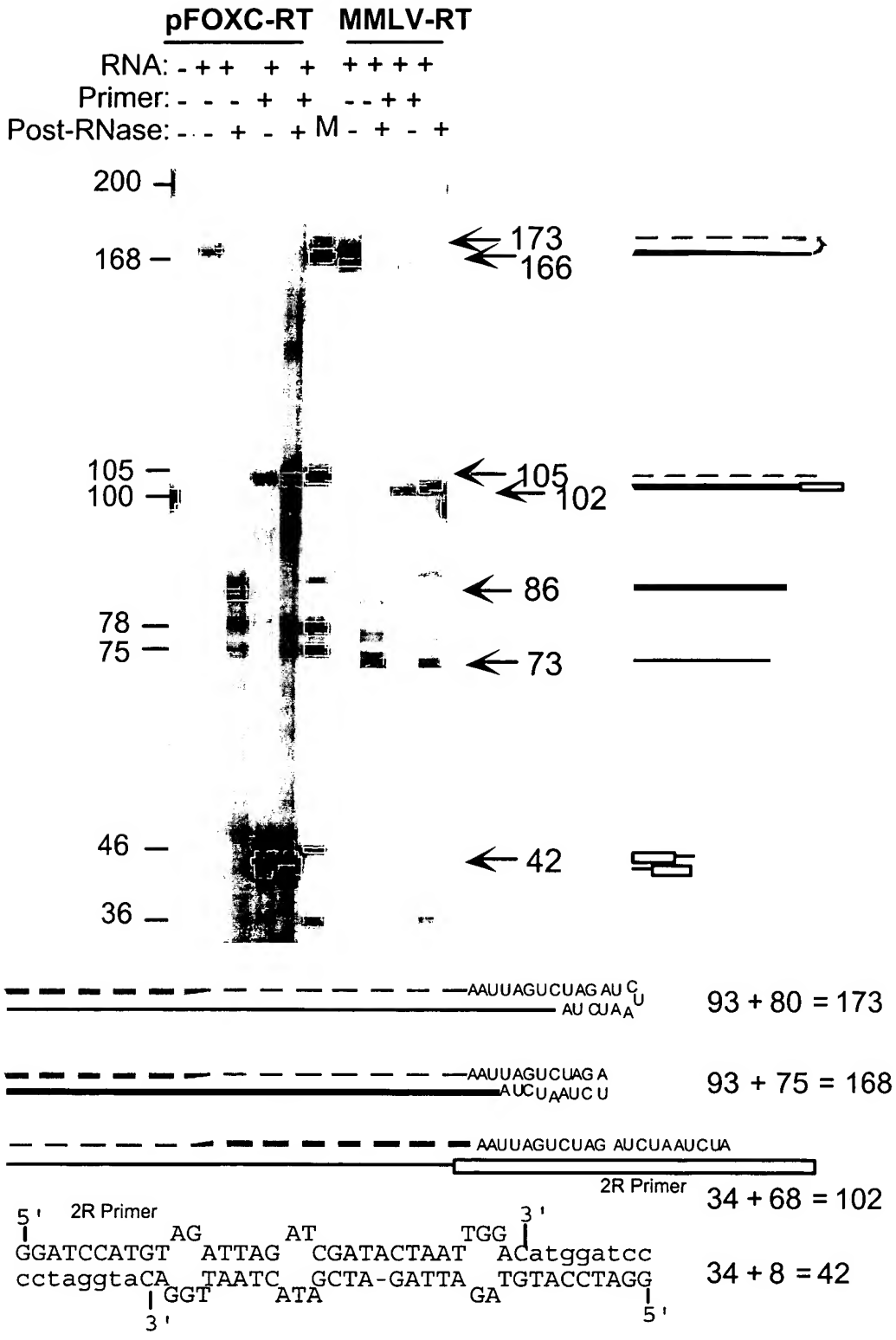
Figure 8



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